

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10529592 and Search Result 20081001_131042_20081001_131042_us-10-529-592a-2.rst.

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GenCore version 6.2.1
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OM protein - nucleic search, using frame_plus_p2n model

```
Run on:      October 1, 2008, 13:10:54 ; Search time 5913 Seconds
              (without alignments)
              1115.322 Million cell updates/sec
```

```
Title:          US-10-529-592A-2
Perfect score:  411
Sequence:       1 MGLKMSCLKGFQMCVSSSSS.....TVWLDETGSCPDDGEIDPEA 76
```

```
Scoring table:  BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop   6.0 , Delext  7.0
```

Searched: 74238366 seqs, 43387191147 residues

Total number of hits satisfying chosen parameters: 148475070

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Command line parameters:
-THR=4 -MODEL=frame+_p2n.model -DEV=SOFT
-Q=/abss/ABSSWEB_spool/US10529592/runat_01102008_131042_15783/app_query.
fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -SIMRANGE=0.0005 -MINMATCH=0.1 -LOOPCL=0
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=0 -MINLEN=0 -MAXLEN=2000000000
-MINDBSEQLLEN=1 -HOST=ai3-01
-USER=US10529592_@CGN_1_1_3128_@runat_01102008_131042_15783 -NCPU=6 -NO_MMAP
-NEG_SCORES=0 -WAIT -LONGLOG -MINDIST=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_est13:*
12: gb_est12:*
13: gb_est11:*
14: gb_est10:*
15: gb_est14:*
16: gb_gss1:*
17: gb_gss2:*
18: gb_gss3:*
19: gb_gss4:*
20: gb_gss5:*
21: gb_gss6:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
	1	411	100.0	443	9	CN366258	CN366258	170006008
	2	411	100.0	447	5	CD674248	CD674248	fs08d06.y
	3	411	100.0	843	5	CB993691	CB993691	AGENCOURT
	4	411	100.0	889	3	BQ671560	BQ671560	AGENCOURT
	5	411	100.0	916	4	BU527159	BU527159	AGENCOURT
	6	411	100.0	979	3	BQ672221	BQ672221	AGENCOURT
	7	364	88.6	542	3	BM688675	BM688675	UI-E-CQ1-
	8	353.5	86.0	735	2	BI914593	BI914593	603179545
	9	344	83.7	289	9	CV025223	CV025223	2842 Full

	10	343.5	83.6	524	10	CX593919	CX593919 CT020006B
	11	343.5	83.6	672	10	CX602183	CX602183 CT02031B2
	12	319	77.6	840	2	BI546970	BI546970 603190185
	13	318.5	77.5	509	12	EE819359	EE819359 010914OND
	14	312.5	76.0	266	13	DY221484	DY221484 000828BEM
	15	312.5	76.0	465	13	DY097784	DY097784 001018BEM
	16	312.5	76.0	513	2	BF043070	BF043070 BP250018A
	17	312.5	76.0	539	10	CX735826	CX735826 783106 MA
	18	312.5	76.0	743	9	CO889561	CO889561 BovGen_17
	19	312.5	76.0	803	9	CR850184	CR850184 CR850184
	20	311	75.7	792	4	BX915255	BX915255 BX915255
	21	311	75.7	1094	3	BM925906	BM925906 AGENCOURT
c	22	309.5	75.3	786	10	CX952215	CX952215 UMC-bemiv
c	23	309.5	75.3	790	10	CX952210	CX952210 UMC-bemiv
	24	309	75.2	317	7	AV498540	AV498540 AV498540
	25	309	75.2	350	17	CG537326	CG537326 OST126203
	26	309	75.2	362	7	AV492641	AV492641 AV492641
	27	309	75.2	394	17	CG492275	CG492275 OST30012
	28	309	75.2	489	17	CG596732	CG596732 OST259293
	29	309	75.2	496	17	CG596379	CG596379 OST258179
	30	309	75.2	503	7	AV505513	AV505513 AV505513
	31	309	75.2	504	17	CG608312	CG608312 OST288313
	32	309	75.2	524	4	BX513871	BX513871 BX513871
	33	309	75.2	529	17	CG612861	CG612861 OST299459
	34	309	75.2	543	11	EL962847	EL962847 mouse_007
	35	309	75.2	674	2	BF472374	BF472374 UI-M-BH3-
	36	309	75.2	682	6	AK004494	AK004494 Mus muscu
	37	309	75.2	683	5	BY704719	BY704719 BY704719
	38	309	75.2	687	10	CX224265	CX224265 MNS41385
	39	309	75.2	698	3	BQ746342	BQ746342 UI-M-ER0-
	40	309	75.2	728	9	CO797158	CO797158 AGENCOURT
	41	309	75.2	759	9	CO795048	CO795048 AGENCOURT
	42	309	75.2	805	9	CO803402	CO803402 AGENCOURT
	43	308	74.9	568	17	CG519452	CG519452 OST82932
	44	304	74.0	460	7	AW918838	AW918838 EST350142
c	45	304	74.0	730	9	CK842592	CK842592 UI-R-BJ1-

ALIGNMENTS

RESULT 1

CN366258

LOCUS CN366258 443 bp mRNA linear EST 16-MAY-2004

DEFINITION 17000600846626 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN366258

VERSION CN366258.1 GI:47366192

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 443)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197

COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 443 Std Error: 0.00.

FEATURES Location/Qualifiers
source 1. .443
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEU"
/note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e-38	Length:	443
Score:	411.00	Matches:	76
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	9	Gaps:	0

US-10-529-592A-2 (1-76) x CN366258 (1-443)

Qy 1 MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer 20
|||||
Db 40 ATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGC 99

Qy 21 SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle 40
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Db 100 AGCCACGACGAGGCCCGCTCCTGAACGACAAGCACCTGGACGTGCCCCGACATCATCATC 159

Qy 41 ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu 60
|||||

Db 160 ACGCCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTG 219

Qy 61 AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla 76
|||||

Db 220 GATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC 267

RESULT 2

CD674248

LOCUS CD674248 447 bp mRNA linear EST 24-JUN-2003

DEFINITION fs08d06.y1 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone fs08d06 5', mRNA sequence.

ACCESSION CD674248

VERSION CD674248.1 GI:32175979

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 447)

AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

TITLE Expressed sequence tag analysis of adult human lens for the NEIBank Project: over 2000 non-redundant transcripts, novel genes and splice variants

JOURNAL Mol. Vis. 8 (4), 171-184 (2002)

PUBMED 12107413

COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
7/201, NIH, Bethesda, MD 20892-0703, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 08 row: d column: 06
Seq primer: M13RP1 reverse primer (ABI).

FEATURES Location/Qualifiers
source 1. .447
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fs08d06"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"

/clone_lib="Human Lens cDNA (Normalized): fs"
/note="Organ: Eye; Vector: pCMVSPORT6; A human lens library (by) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (C0t 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center(NISC)."

ORIGIN

Alignment Scores:

Pred. No.:	3.87e-38	Length:	447
Score:	411.00	Matches:	76
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-529-592A-2 (1-76) x CD674248 (1-447)

Qy	1	MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer	20
Db	177	ATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGC	236
Qy	21	SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle	40
Db	237	AGCCACGACGAGGCCCGTCCTGAACGACAAGCACCTGGACGTGCCCCACATCATCATC	296
Qy	41	ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu	60
Db	297	ACGCCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTG	356
Qy	61	AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla	76
Db	357	GATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC	404

RESULT 3

CB993691

LOCUS	CB993691	843 bp	mRNA	linear	EST 01-MAY-2003
DEFINITION	AGENCOURT_13624626 NIH_MGC_148 Homo sapiens cDNA clone IMAGE:30338285 5', mRNA sequence.				
ACCESSION	CB993691				

VERSION

CB993691.1

GI:30288211

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 843)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cdna Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: NDAM364 row: 1 column: 06

High quality sequence stop: 408.

FEATURES

Location/Qualifiers

source

1. .843

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30338285"

/tissue_type="pre-eclamptic placenta"

/lab_host="DH10B TonA"

/clone_lib="NIH_MGC_148"

/note="Organ: placenta; Vector: pBluescriptR; Site_1:
alI-XhoI; Site_2: BamH; Library is oligo-dT primed and directionally cloned using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	8.39e-38	Length:	843
Score:	411.00	Matches:	76
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0

Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-529-592A-2 (1-76) x CB993691 (1-843)

Qy	1	MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer	20
Db	185	ATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGC	244
Qy	21	SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle	40
Db	245	AGCCACGACGAGGCCCGCTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATC	304
Qy	41	ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu	60
Db	305	ACGCCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTG	364
Qy	61	AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla	76
Db	365	GATGAGACAGGGTCGTGCCCAGATGATGGAGAAATTGACCCAGAAGCC	412

RESULT 4

BQ671560

LOCUS	BQ671560	889 bp	mRNA	linear	EST 15-JUL-2002
DEFINITION	AGENCOURT_8171941 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6277428 5', mRNA sequence.				
ACCESSION	BQ671560				
VERSION	BQ671560.1 GI:21782394				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 889)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2463 row: m column: 13 High quality sequence stop: 549.				

Location/Qualifiers

source

1.889

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/organism="Homo sapiens"
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/mol_type="mRNA"

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/db xref="taxon:9606"
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/clone="IMAGE:6277428"
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/tissue_type="epidermoid carcinoma, cell line"
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```
/lab host="DH10B (phage-resistant)"
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/clone lib="NIH MGC 102"
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/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
```

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	8.95e-38	Length:	889
Score:	411.00	Matches:	76
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-529-592A-2 (1-76) x B0671560 (1-889)

Qy		1 MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSer	20
Db	185	ATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGC	244
Qy		21 SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle	40
Db	245	AGCCACGACGAGGCCCGTCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATC	304
Qy		41 ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu	60
Db	305	ACGCCCCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTG	364
Qy		61 AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla	76
Db	365	GATGAGACAGGGTCGTGCCCAGATGATGGAGAAAATCGACCCAGAAGCC	412

RESULT 5

BU527159

LOCUS	BU527159	916 bp	mRNA	linear	EST 13-SEP-2002
-------	----------	--------	------	--------	-----------------

DEFINITION AGENCOURT_10154878 NIH_MGC_101 Homo sapiens cDNA clone

IMAGE:6536921 5', mRNA sequence.

ACCESSION BU527159

VERSION BU527159.1 GI:22837600

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 916)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2699 row: a column: 17
High quality sequence stop: 653.

FEATURES Location/Qualifiers

source 1. .916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6536921"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	9.28e-38	Length:	916
Score:	411.00	Matches:	76
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0

DB: 4 Gaps: 0

US-10-529-592A-2 (1-76) x BU527159 (1-916)

Qy	1	MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer	20
Db	165	ATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGC	224
Qy	21	SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle	40
Db	225	AGCCACGACGAGGCCCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATC	284
Qy	41	ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu	60
Db	285	ACGCCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTG	344
Qy	61	AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla	76
Db	345	GATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC	392

RESULT 6
BQ672221
LOCUS BQ672221 979 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8303632 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6274816
5', mRNA sequence.
ACCESSION BQ672221
VERSION BQ672221.1 GI:21783055
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 979)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2456 row: p column: 17
High quality sequence stop: 550.
FEATURES Location/Qualifiers

source 1. .979
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6274816"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.01e-37	Length:	979
Score:	411.00	Matches:	76
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-529-592A-2 (1-76) x BQ672221 (1-979)

Qy	1	MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer	20
Db	185	ATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGC	244
Qy	21	SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle	40
Db	245	AGCCACGACGAGGCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATC	304
Qy	41	ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu	60
Db	305	ACGCCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTG	364
Qy	61	AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla	76
Db	365	GATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC	412

RESULT 7

BM688675

LOCUS BM688675 542 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-CQ1-acq-e-11-0-UI.r1 UI-E-CQ1 Homo sapiens cDNA clone
UI-E-CQ1-acq-e-11-0-UI 5', mRNA sequence.

ACCESSION BM688675
 VERSION BM688675.1 GI:19001933
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 542)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Cancer Biology & Epigenomics Program
 Children's Memorial Research Center
 2300 Children's Plaza, Box 220, Chicago, IL 60614-3394, USA
 Tel: 773 755 6551
 Fax: 773 755 6378
 Email: mbsoares@childrensmemorial.org
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Reverse.
 FEATURES
 source Location/Qualifiers
 1. .542
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-CQ1-acq-e-11-0-UI"
 /tissue_type="optic nerve"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-CQ1"
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 UI-E-CQ1 is a normalized cDNA library containing the
 following tissue(s): optic nerve. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Alignment Scores:

Pred. No.:	1.78e-32	Length:	542
Score:	364.00	Matches:	67
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	88.6%	Indels:	0
DB:	3	Gaps:	0

US-10-529-592A-2 (1-76) x BM688675 (1-542)

Qy	10	GlyPheGlnMetCysValSerSerSerSerSerSerHisAspGluAlaProValLeuAsn	29
Db	44	GGCTTTCAAATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCGTCCTGAAC	103
Qy	30	AspLysHisLeuAspValProAspIleIleIleThrProProThrProThrGlyMetMet	49
Db	104	GACAAGCACCTGGACGTGCGGACATCATCATCACGCCCCCACCCACGGGCATGATG	163
Qy	50	LeuProArgAspLeuGlySerThrValTrpLeuAspGluThrGlySerCysProAspAsp	69
Db	164	CTGCCGAGGGACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGAT	223
Qy	70	GlyGluIleAspProGluAla	76
Db	224	GGAGAAATCGACCCAGAAGCC	244

RESULT 8

BI914593

LOCUS BI914593 735 bp mRNA linear EST 16-OCT-2001

DEFINITION 603179545F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243626 5', mRNA sequence.

ACCESSION BI914593

VERSION BI914593.1 GI:16178714

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 735)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11614 row: j column: 11
High quality sequence stop: 723.
FEATURES Location/Qualifiers
source 1. .735
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5243626"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	4.51e-31	Length:	735
Score:	353.50	Matches:	68
Percent Similarity:	89.5%	Conservative:	0
Best Local Similarity:	89.5%	Mismatches:	1
Query Match:	86.0%	Indels:	7
DB:	2	Gaps:	1

US-10-529-592A-2 (1-76) x BI914593 (1-735)

Qy	1	MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer	20
Db	45	ATGGGGCTTAAGATGTCCTGCCTGAAA-----TGCAGCAGCAGC	83
Qy	21	SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle	40
Db	84	AGCCACGACGAGGCCCGTCCTGAACGACAAGCACCTGGACGTGCCCGACATCATCATC	143

Qy	41	ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu	60
Db	144	ACGCCCCCACCCCCACGGGCATGATGCTGCCGAGGGACTTGGGGAGCACAGTCTGGCTG	203
Qy	61	AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla	76
Db	204	GATGAGACAGGGTCGTGCCCAGATGATGGAGAAATCGACCCAGAAGCC	251

POLYA=No.

FEATURES Location/Qualifiers
 source 1. .289
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="mixed"
 /clone_lib="Full Length cDNA from the Mammalian Gene
 Collection"
 /note="Vector: mixed; The ORFs were PCR amplified from the
 MGC (Mammalian Gene Collection) and cloned by
 recombinational Gateway cloning into pDONR223 Donor
 vector. Reference : MGC (Mammalian Gene Collection)
 Program Team, Generation and Initial Analysis of more than
 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
 2002, 99(26), 16899-16903"

ORIGIN

Alignment Scores:

Pred. No.:	1.92e-30	Length:	289
Score:	344.00	Matches:	63
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	98.4%	Mismatches:	0
Query Match:	83.7%	Indels:	0
DB:	9	Gaps:	0

US-10-529-592A-2 (1-76) x CV025223 (1-289)

Qy	13	MetCysValSerSerSerSerSerSerHisAspGluAlaProValLeuAsnAspLysHis	32
Db	1	ATGTGTGTCAGCAGCAGCAGCAGCAGCCACGACGAGGCCCGTCCTGAACGACAAGCAC	60
Qy	33	LeuAspValProAspIleIleIleThrProProThrProThrGlyMetMetLeuProArg	52
Db	61	CTGGACGTGCCCCGACATCATCATCACGCCCCCACCCCCACGGGCATGATGCTGCCGAGG	120
Qy	53	AspLeuGlySerThrValTrpLeuAspGluThrGlySerCysProAspAspGlyGluIle	72
Db	121	GACTTGGGGAGCACAGTCTGGCTGGATGAGACAGGGTCGTGCCCAGATGATGGAGAAATC	180
Qy	73	AspProGluAla	76
		:::	
Db	181	GACCCAGAATCC	192

RESULT 10

CX593919

LOCUS CX593919 524 bp mRNA linear EST 13-JAN-2005
DEFINITION CT020006B20F11 Equine Articular Cartilage cDNA Library Equus
 caballus cDNA clone CT020006B20F11, mRNA sequence.

ACCESSION CX593919
VERSION CX593919.1 GI:57700847
KEYWORDS EST.
SOURCE Equus caballus (horse)
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 524)
AUTHORS MacLeod, J.N.
TITLE Expressed sequence tags from a normalized equine articular
cartilage cDNA library
JOURNAL Unpublished (2005)
COMMENT Contact: MacLeod JN
Department of Veterinary Science
University of Kentucky
Gluck Equine Research Center, Lexington, KY 40546-0099, USA
Tel: 859.257.4757
Fax: 859.257.8542
Email: jnmacleod@uky.edu
High quality sequence stop: 524.

FEATURES Location/Qualifiers
source 1..524
/organism="Equus caballus"
/mol_type="mRNA"
/strain="Thoroughbred"
/db_xref="taxon:9796"
/clone="CT020006B20F11"
/sex="male"
/tissue_type="articular cartilage"
/dev_stage="1.5 year old"
/lab_host="DH12S E. Coli cells (Invitrogen)"
/clone_lib="Equine Articular Cartilage cDNA Library"
/note="Vector: pGEM11Zf(+) (Promega); Site_1: EcoR1;
Site_2: NotI"

ORIGIN

Alignment Scores:

Pred. No.:	4.55e-30	Length:	524
Score:	343.50	Matches:	65
Percent Similarity:	92.1%	Conservative:	5
Best Local Similarity:	85.5%	Mismatches:	5
Query Match:	83.6%	Indels:	1
DB:	10	Gaps:	1

US-10-529-592A-2 (1-76) x CX593919 (1-524)

Qy	1	MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer	20
		::: :::	
Db	28	ATGGGGCTGAAGCTGTCCTGCCTGAAAGGCCTTAAAATGTGTGTC---AGCAGCAGCAGC	84

```
Qy      21  SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle  40
        |||||||||||||||||||||||||||:~:~:|||||||||||||||||||||:~:~:|||||
Db      85  AGCCACGACGAGGCCCGCTTCTGAGCGACAAGCACCTGGATGTACCCAACATCATCATT 144

Qy      41  ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu  60
        |||||||||||||||||||||||||||          |||||||||||
Db     145  ACTCCCCCTACCCCCACGGGCATGATGCTGCCAAGGGACTCCAGGCAGACAGTCTGGCTG 204

Qy      61  AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla  76
        ||||||||||||||||~:~:|||||||||||||||||
Db     205  GATGAGACGGGGTCCTGCACAGAGGATGGGGAAATAGACCCCGAAGCC 252
```

RESULT 11

CX602183

LOCUS CX602183 672 bp mRNA linear EST 13-JAN-2005

DEFINITION CT02031B2H06 Equine Articular Cartilage cDNA Library Equus caballus
cDNA clone CT02031B2H06, mRNA sequence.

ACCESSION CX602183

VERSION CX602183.1 GI:57717395

KEYWORDS EST.

SOURCE Equus caballus (horse)

ORGANISM Equus caballus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.

REFERENCE 1 (bases 1 to 672)

AUTHORS MacLeod, J.N.

TITLE Expressed sequence tags from a normalized equine articular
cartilage cDNA library

JOURNAL Unpublished (2005)

COMMENT Contact: MacLeod JN
Department of Veterinary Science
University of Kentucky
Gluck Equine Research Center, Lexington, KY 40546-0099, USA
Tel: 859.257.4757
Fax: 859.257.8542
Email: jnmacleod@uky.edu
High quality sequence stop: 672.

FEATURES Location/Qualifiers

source 1..672
/organism="Equus caballus"
/mol_type="mRNA"
/strain="Thoroughbred"
/db_xref="taxon:9796"
/clone="CT02031B2H06"
/sex="male"
/tissue_type="articular cartilage"
/dev_stage="1.5 year old"
/lab_host="DH12S E. Coli cells (Invitrogen)"

```

/clone_lib="Equine Articular Cartilage cDNA Library"
/note="Vector: pGEM11zf(+) (Promega); Site_1: EcoR1;
Site_2: NotI"

```

ORIGIN

Alignment Scores:

Pred. No.:	6.16e-30	Length:	672
Score:	343.50	Matches:	65
Percent Similarity:	92.1%	Conservative:	5
Best Local Similarity:	85.5%	Mismatches:	5
Query Match:	83.6%	Indels:	1
DB:	10	Gaps:	1

US-10-529-592A-2 (1-76) x CX602183 (1-672)

Qy	1	MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer	20
		:::	
Db	185	ATGGGGCTGAAGCTGTCCTGCCTGAAAGGCCTTAAAATGTGTGTC---AGCAGCAGCAGC	241
Qy	21	SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle	40
		:::	
Db	242	AGCCACGACGAGGCCCGTTCTGAGCGACAAGCACCTGGATGTACCCAACATCATCATT	301
Qy	41	ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu	60
Db	302	ACTCCCCCTACCCCCACGGGCATGATGCTGCCAAGGGACTCCAGGCAGACAGTCTGGCTG	361
Qy	61	AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla	76
		:::	
Db	362	GATGAGACGGGGTCCTGCACAGAGGATGGGGAAATAGACCCCGAAGCC	409

RESULT 12

BI546970

LOCUS BI546970 840 bp mRNA linear EST 05-SEP-2001

DEFINITION 603190185F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5261660 5', mRNA sequence.

ACCESSION BI546970

VERSION BI546970.1 GI:15434282

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 840)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11659 row: i column: 21
High quality sequence stop: 737.

FEATURES Location/Qualifiers
source 1. .840
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5261660"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_95"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
 (gtcgag); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.5 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: this
 is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	6.41e-27	Length:	840
Score:	319.00	Matches:	70
Percent Similarity:	78.0%	Conservative:	1
Best Local Similarity:	76.9%	Mismatches:	5
Query Match:	77.6%	Indels:	16
DB:	2	Gaps:	3

US-10-529-592A-2 (1-76) x BI546970 (1-840)

Qy	1	MetGlyLeuLysMetSerCysLeuLys-----GlyPheGlnMet-----	13
			:::
Db	211	ATGGGGCTTAAGATGTCCTGCCTGAAAGACGCCGGTTTTTCATCTGTGATGCGGGGACAGC	270
Qy	14	CysVal-----SerSerSerSerSerSerHisAspGluAlaPro	26
Db	271	TGCGCTCCTTGCTGCGAGGCGTCAGGACCCAGCAGCAGCAGCAGCCACGACGAGGCCCCC	330

http://es/ScoreAccessWeb/GetItem.action?AppId=105295...1_131042_us-10-529-592a-2.rst&ItemType=4&startByte=0 (22 of 26)10/6/2008 9:36:29 AM


```
FEATURES                                Location/Qualifiers
     source                             1. .266
                                         /organism="Bos taurus"
                                         /mol_type="mRNA"
                                         /db_xref="taxon:9913"
                                         /tissue_type="Life Tech Normalised library"
                                         /clone_lib="BEMN"
                                         /note="Vector: pCMV-Sport6; Life Tech Normalised library"
```

ORIGIN

Alignment Scores:

Pred. No.:	9.28e-27	Length:	266
Score:	312.50	Matches:	57
Percent Similarity:	88.2%	Conservative:	10
Best Local Similarity:	75.0%	Mismatches:	8
Query Match:	76.0%	Indels:	1
DB:	13	Gaps:	1

US-10-529-592A-2 (1-76) x DY221484 (1-266)

Qy	1 MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer 20 : : : : : : :
Db	39 ATGGGGCTGAAGCTGACCTGCCTGAAAGGCTTAAAGATGTGTGTA---AGCAGCAGTGGC 95
Qy	21 SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle 40 : : : :
Db	96 AGCCACGACGAGGCCCGCTGCTGAGCGACAAGCACCTGGACGTCCCCAACATCATCATC 155
Qy	41 ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu 60 : :
Db	156 ACGCCGCCGACCCCCACAGGTGTGGCCCTGCCCAGGGACACCCGGAGGGCAGTCTGGCTG 215
Qy	61 AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla 76 : : : : : : : : : :
Db	216 GACGAGTCTGGGTCGTGCACGGAGGATGGAGACCTTGACCCTGAGGCC 263

RESULT 15

```

DY097784
LOCUS          DY097784                465 bp      mRNA      linear      EST 31-JAN-2006
DEFINITION    001018BEMN049915HT BEMN Bos taurus cDNA, mRNA sequence.
ACCESSION     DY097784
VERSION       DY097784.1   GI:86244371
KEYWORDS      EST.
SOURCE        Bos taurus (cattle)
  ORGANISM    Bos taurus

```


FEATURES	Location/Qualifiers
source	1. .465 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="Life Tech Normalised library" /clone_lib="BEMN" /note="Vector: pCMV-Sport6; Life Tech Normalised library"

Alignment Scores:

Pred. No.:	1.83e-26	Length:	465
Score:	312.50	Matches:	57
Percent Similarity:	88.2%	Conservative:	10
Best Local Similarity:	75.0%	Mismatches:	8
Query Match:	76.0%	Indels:	1
DB:	13	Gaps:	1

US-10-529-592A-2 (1-76) x DY097784 (1-465)

Qy	1	MetGlyLeuLysMetSerCysLeuLysGlyPheGlnMetCysValSerSerSerSerSer	20
		::: :::	
Db	83	ATGGGGCTGAAGCTGACCTGCCTGAAAGGCTTAAAGATGTGTGTA---AGCAGCAGTGGC	139
Qy	21	SerHisAspGluAlaProValLeuAsnAspLysHisLeuAspValProAspIleIleIle	40
		::: :::	
Db	140	AGCCACGACGAGGCCCGTGCTGAGCGACAAGCACCTGGACGTCCCAACATCATCATC	199
Qy	41	ThrProProThrProThrGlyMetMetLeuProArgAspLeuGlySerThrValTrpLeu	60
		:::	

Db	200	ACGCCGCCGACCCCCACAGGTGTGGCCCTGCCCAGGGACACCCGGAGGGCAGTCTGGCTG	259
Qy	61	AspGluThrGlySerCysProAspAspGlyGluIleAspProGluAla	76
		::: ::: :~::~:	
Db	260	GACGAGTCTGGGTCGTGCACGGAGGATGGAGACCTTGACCCTGAGGCC	307

Search completed: October 1, 2008, 15:15:39
Job time : 5920.96 secs

SCOPE 5.0